

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/522,277
Source: IFW16
Date Processed by STIC: 03/14/2007

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/14/2007

PATENT APPLICATION: US/10/522,277

TIME: 11:06:37

Input Set : N:\SSLM\10522277.txt

Output Set: N:\CRF4\03142007\J522277.raw

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3 <110> APPLICANT: MIZUTANI, Shuki
4   YAMADA, Takayuki
6 <120> TITLE OF INVENTION: Transcription regulating factors
8 <130> FILE REFERENCE: SEN-A0122P
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/522,277
C--> 11 <141> CURRENT FILING DATE: 2005-01-24
13 <150> PRIOR APPLICATION NUMBER: JP 2002-217233
14 <151> PRIOR FILING DATE: 2002-07-25
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2684
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (37)..(2601)
29 <400> SEQUENCE: 1
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31                               Met Val Val Met Ala Arg
32                               1           5
34 ctt tcg cgg ccc gag cgg ccg gac ctt gtc ttc gag gaa gag gac ctc 102
35 Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu Glu Asp Leu
36           10           15           20
38 ccc tat gag gag gaa atc atg cgg aac caa ttc tct gtc aaa tgc tgg 150
39 Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val Lys Cys Trp
40           25           30           35
42 ctt cgc tac atc gag ttc aaa cag ggc gcc ccg aag ccc agg ctc aat 198
43 Leu Arg Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro Arg Leu Asn
44           40           45           50
46 cag cta tac gag cgg gca ctc aag ctg ctg ccc tgc agc tac aaa ctc 246
47 Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser Tyr Lys Leu
48 55           60           65           70
50 tgg tac cga tac ctg aag gcg cgt cgg gca cag gtg aag cat cgc tgt 294
51 Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys His Arg Cys
52           75           80           85
54 gtg acc gac cct gcc tat gaa gat gtc aac aac tgt cat gag agg gcc 342
55 Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His Glu Arg Ala
56           90           95           100
58 ttt gtg ttc atg cac aag atg cct cgt ctg tgg cta gat tac tgc cag 390
59 Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp Tyr Cys Gln
60           105           110           115
62 ttc ctc atg gac cag ggg cgc gtc aca cac acc cgc cgc acc ttc gac 438

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63	Phe	Leu	Met	Asp	Gln	Gly	Arg	Val	Thr	His	Thr	Arg	Arg	Thr	Phe	Asp	
64		120					125					130					
66	cgt	gcc	ctc	cgg	gca	ctg	ccc	atc	acg	cag	cac	tct	cga	att	tgg	ccc	486
67	Arg	Ala	Leu	Arg	Ala	Leu	Pro	Ile	Thr	Gln	His	Ser	Arg	Ile	Trp	Pro	
68	135					140					145					150	
70	ctg	tat	ctg	cgc	ttc	ctg	cgc	tca	cac	cca	ctg	cct	gag	aca	gct	gtg	534
71	Leu	Tyr	Leu	Arg	Phe	Leu	Arg	Ser	His	Pro	Leu	Pro	Glu	Thr	Ala	Val	
72				155						160						165	
74	cga	ggc	tat	cgg	cgc	ttc	ctc	aag	ctg	agt	cct	gag	agt	gca	gag	gag	582
75	Arg	Gly	Tyr	Arg	Arg	Phe	Leu	Lys	Leu	Ser	Pro	Glu	Ser	Ala	Glu	Glu	
76				170						175				180			
78	tac	att	gag	tac	ctc	aag	tca	agt	gac	cgg	ctg	gat	gag	gcc	gcc	cag	630
79	Tyr	Ile	Glu	Tyr	Leu	Lys	Ser	Ser	Asp	Arg	Leu	Asp	Glu	Ala	Ala	Gln	
80			185							190				195			
82	cgc	ctg	gcc	acc	gtg	gtg	aac	gac	gag	cgt	ttc	gtg	tct	aag	gcc	ggc	678
83	Arg	Leu	Ala	Thr	Val	Val	Asn	Asp	Glu	Arg	Phe	Val	Ser	Lys	Ala	Gly	
84	200						205					210					
86	aag	tcc	aac	tac	cag	ctg	tgg	cac	gag	ctg	tgc	gac	ctc	atc	tcc	cag	726
87	Lys	Ser	Asn	Tyr	Gln	Leu	Trp	His	Glu	Leu	Cys	Asp	Leu	Ile	Ser	Gln	
88	215				220						225					230	
90	aat	ccg	gac	aag	gta	cag	tcc	ctc	aat	gtg	gac	gcc	atc	atc	cgc	ggg	774
91	Asn	Pro	Asp	Lys	Val	Gln	Ser	Leu	Asn	Val	Asp	Ala	Ile	Ile	Arg	Gly	
92				235						240					245		
94	ggc	ctc	acc	cgc	ttc	acc	gac	cag	ctg	ggc	aag	ctc	tgg	tgt	tct	ctc	822
95	Gly	Leu	Thr	Arg	Phe	Thr	Asp	Gln	Leu	Gly	Lys	Leu	Trp	Cys	Ser	Leu	
96				250						255				260			
98	gcc	gac	tac	tac	atc	cgc	agc	ggc	cat	ttc	gag	aag	gct	cgg	gac	gtg	870
99	Ala	Asp	Tyr	Tyr	Ile	Arg	Ser	Gly	His	Phe	Glu	Lys	Ala	Arg	Asp	Val	
100			265					270					275				
102	tac	gag	gag	gcc	atc	cgg	aca	gtg	atg	acc	gtg	cgg	gac	ttc	aca	cag	918
103	Tyr	Glu	Glu	Ala	Ile	Arg	Thr	Val	Met	Thr	Val	Arg	Asp	Phe	Thr	Gln	
104			280				285						290				
106	gtg	ttt	gac	agc	tac	gcc	cag	ttc	gag	gag	agc	atg	atc	gct	gca	aag	966
107	Val	Phe	Asp	Ser	Tyr	Ala	Gln	Phe	Glu	Glu	Ser	Met	Ile	Ala	Ala	Lys	
108	295				300						305					310	
110	atg	gag	acc	gcc	tgc	gag	ctg	ggg	cgc	gag	gag	gag	gat	gat	gtg	gac	1014
111	Met	Glu	Thr	Ala	Ser	Glu	Leu	Gly	Arg	Glu	Glu	Glu	Asp	Asp	Val	Asp	
112				315						320					325		
114	ctg	gag	ctg	cgc	ctg	gcc	cgc	ttc	gag	cag	ctc	atc	agc	cgg	cgg	ccc	1062
115	Leu	Glu	Leu	Arg	Leu	Ala	Arg	Phe	Glu	Gln	Leu	Ile	Ser	Arg	Arg	Pro	
116				330						335				340			
118	ctg	ctc	ctc	aac	agc	gtc	ttg	ctg	cgc	caa	aac	cca	cac	cac	gtg	cac	1110
119	Leu	Leu	Leu	Asn	Ser	Val	Leu	Leu	Arg	Gln	Asn	Pro	His	His	Val	His	
120			345					350						355			
122	gag	tgg	cac	aag	cgt	gtc	gcc	ctg	cac	cag	ggc	cgc	ccc	cgg	gag	atc	1158
123	Glu	Trp	His	Lys	Arg	Val	Ala	Leu	His	Gln	Gly	Arg	Pro	Arg	Glu	Ile	
124		360					365					370					
126	atc	aac	acc	tac	aca	gag	gct	gtg	cag	acg	gtg	gac	ccc	ttc	aag	gcc	1206
127	Ile	Asn	Thr	Tyr	Thr	Glu	Ala	Val	Gln	Thr	Val	Asp	Pro	Phe	Lys	Ala	

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128	375					380					385				390		
130	aca	ggc	aag	ccc	cac	act	ctg	tgg	gtg	gcg	ttt	gcc	aag	ttt	tat	gag	1254
131	Thr	Gly	Lys	Pro	His	Thr	Leu	Trp	Val	Ala	Phe	Ala	Lys	Phe	Tyr	Glu	
132					395					400					405		
134	gac	aac	gga	cag	ctg	gac	gat	gcc	cgt	gtc	atc	ctg	gag	aag	gcc	acc	1302
135	Asp	Asn	Gly	Gln	Leu	Asp	Asp	Ala	Arg	Val	Ile	Leu	Glu	Lys	Ala	Thr	
136				410					415					420			
138	aag	gtg	aac	ttc	aag	cag	gtg	gat	gac	ctg	gca	agc	gtg	tgg	tgt	cag	1350
139	Lys	Val	Asn	Phe	Lys	Gln	Val	Asp	Asp	Leu	Ala	Ser	Val	Trp	Cys	Gln	
140				425					430					435			
142	tgc	gga	gag	ctg	gag	ctc	cga	cac	gag	aac	tac	gat	gag	gcc	ttg	cgg	1398
143	Cys	Gly	Glu	Leu	Glu	Leu	Arg	His	Glu	Asn	Tyr	Asp	Glu	Ala	Leu	Arg	
144		440						445					450				
146	ctg	ctg	cga	aag	gcc	acg	gcg	ctg	cct	gcc	cgc	cgg	gcc	gag	tac	ttt	1446
147	Leu	Leu	Arg	Lys	Ala	Thr	Ala	Leu	Pro	Ala	Arg	Arg	Ala	Glu	Tyr	Phe	
148	455					460					465					470	
150	gat	ggt	tca	gag	ccc	gtg	cag	aac	cgc	gtg	tac	aag	tca	ctg	aag	gtc	1494
151	Asp	Gly	Ser	Glu	Pro	Val	Gln	Asn	Arg	Val	Tyr	Lys	Ser	Leu	Lys	Val	
152					475					480					485		
154	tgg	tcc	atg	ctc	gcc	gac	ctg	gag	gag	agc	ctc	ggc	acc	ttc	cag	tcc	1542
155	Trp	Ser	Met	Leu	Ala	Asp	Leu	Glu	Glu	Ser	Leu	Gly	Thr	Phe	Gln	Ser	
156				490					495					500			
158	acc	aag	gcc	gtg	tac	gac	cgc	atc	ctg	gac	ctg	cgt	atc	gca	aca	ccc	1590
159	Thr	Lys	Ala	Val	Tyr	Asp	Arg	Ile	Leu	Asp	Leu	Arg	Ile	Ala	Thr	Pro	
160				505					510					515			
162	cag	atc	gtc	atc	aac	tat	gcc	atg	ttc	ctg	gag	gag	cac	aag	tac	ttc	1638
163	Gln	Ile	Val	Ile	Asn	Tyr	Ala	Met	Phe	Leu	Glu	Glu	His	Lys	Tyr	Phe	
164		520					525					530					
166	gag	gag	agc	ttc	aag	gcg	tac	gag	cgc	ggc	atc	tcg	ctg	ttc	aag	tgg	1686
167	Glu	Glu	Ser	Phe	Lys	Ala	Tyr	Glu	Arg	Gly	Ile	Ser	Leu	Phe	Lys	Trp	
168	535					540					545					550	
170	ccc	aac	gtg	tcc	gac	atc	tgg	agc	acc	tac	ctg	acc	aaa	ttc	att	gcc	1734
171	Pro	Asn	Val	Ser	Asp	Ile	Trp	Ser	Thr	Tyr	Leu	Thr	Lys	Phe	Ile	Ala	
172					555						560				565		
174	cgc	tat	ggg	ggc	cgc	aag	ctg	gag	cgg	gca	cgg	gac	ctg	ttt	gaa	cag	1782
175	Arg	Tyr	Gly	Gly	Arg	Lys	Leu	Glu	Arg	Ala	Arg	Asp	Leu	Phe	Glu	Gln	
176				570													

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194 cac acc cgc ggc atc tac cag aag gcc att gag gtg ctg tgc gac gag 2022
195 His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu Ser Asp Glu
196      650      655      660
198 cac gcg cgt gag atg tgc ctg cgg ttt gca gac atg gag tgc aag ctc 2070
199 His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu Cys Lys Leu
200      665      670      675
202 ggg gag att gac cgc gcc cgg gcc atc tac agc ttc tgc tcc cag atc 2118
203 Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys Ser Gln Ile
204      680      685      690
206 tgt gac ccc cgg acg acc ggc gcg ttc tgg cag acg tgg aag gac ttt 2166
207 Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp Lys Asp Phe
208 695      700      705      710
210 gag gtc cgg cat ggc aat gag gac acc atc aag gaa atg ctg cgt atc 2214
211 Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met Leu Arg Ile
212      715      720      725
214 cgg cgc agc gtg cag gcc acg tac aac acg cag gtc aac ttc atg gcc 2262
215 Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn Phe Met Ala
216      730      735      740
218 tgc cag atg ctc aag gtc tgc ggc agt gcc acg ggc acc gtg tct gac 2310
219 Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr Val Ser Asp
220      745      750      755
222 ctg gcc cct ggg cag agt ggc atg gac gac atg aag ctg ctg gaa cag 2358
223 Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu Leu Glu Gln
224      760      765      770
226 cgg gca gag cag ctg gcg gct gag gcg gag cgt gac cag ccc ttg cgc 2406
227 Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln Pro Leu Arg
228 775      780      785      790
230 gcc cag agc aag atc ctg ttc gtg agg agt gac gcc tcc cgg gag gag 2454
231 Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser Arg Glu Glu
232      795      800      805
234 ctg gca gag ctg gca cag cag gtc aac ccc gag gag atc cag ctg ggc 2502
235 Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile Gln Leu Gly
236      810      815      820
238 gag gac gag gac gag gac gag atg gac ctg gag ccc aac gag gtt cgg 2550
239 Glu Asp Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn Glu Val Arg
240      825      830      835
242 ctg gag cag cag agc gtg cca gcc gca gtg ttt ggg agc ctg aag gaa 2598
243 Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser Leu Lys Glu
244      840      845      850
246 gac tgacccgtcc ctcccccatc cccctcccc accccctccc caatacagct 2651
247 Asp
248 855
250 acgtttgtac aaaaaaaaaa aaaaaaaaaa aaa 2684
253 <210> SEQ ID NO: 2
254 <211> LENGTH: 855
255 <212> TYPE: PRT
256 <213> ORGANISM: Homo sapiens
258 <400> SEQUENCE: 2
259 Met Val Val Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val

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260      1              5              10              15
262 Phe Glu Glu Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln
263              20              25              30
265 Phe Ser Val Lys Cys Trp Leu Arg Tyr Ile Glu Phe Lys Gln Gly Ala
266              35              40              45
268 Pro Lys Pro Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu
269              50              55              60
271 Pro Cys Ser Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala
272      65              70              75              80
274 Gln Val Lys His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn
275              85              90              95
277 Asn Cys His Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu
278              100             105             110
280 Trp Leu Asp Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His
281              115             120             125
283 Thr Arg Arg Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln
284      130             135             140
286 His Ser Arg Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro
287 145             150             155             160
289 Leu Pro Glu Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser
290              165             170             175
292 Pro Glu Ser Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg
293              180             185             190
295 Leu Asp Glu Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg
296              195             200             205
298 Phe Val Ser Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu
299      210             215             220
301 Cys Asp Leu Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val
302 225             230             235             240
304 Asp Ala Ile Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly
305              245             250             255
307 Lys Leu Trp Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe
308              260             265             270
310 Glu Lys Ala Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr
311              275             280             285
313 Val Arg Asp Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu
314      290             295             300
316 Ser Met Ile Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu
317 305             310             315             320
319 Glu Glu Asp Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln
320              325             330             335
322 Leu Ile Ser Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln
323              340             345             350
325 Asn Pro His His Val His Glu Trp His Lys Arg Val Ala Leu His Gln
326              355             360             365
328 Gly Arg Pro Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr
329      370             375             380
331 Val Asp Pro Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala
332 385             390             395             400

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date